Supplementary Information

Enhancing Oligopeptide-215 Skin Lipid Bilayer Diffusivity via Other Anti-aging Peptide: A Molecular Dynamics Simulation Study

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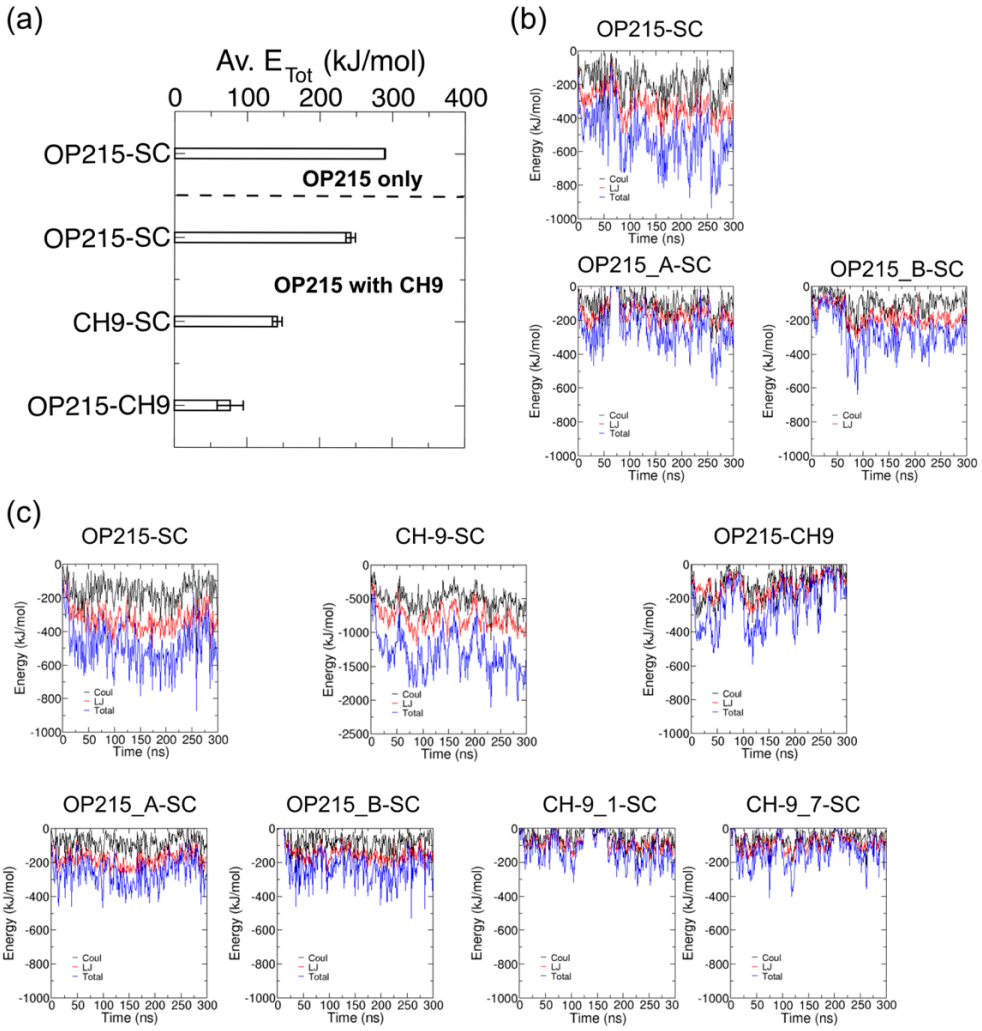


Figure S1. Interaction energies between peptides and SC lipids from each system. (**a**) The total interaction energies (coulombic + dispersive) over the last 100 ns of simulation between peptide and SC lipids (OP215-SC and CH9-SC: averaged over energies between each peptide and SC lipids) or between OP215 and CH9 peptides (OP215-CH9: averaged over energies between each OP215 peptide and CH9 peptides). (**b**) OP215 only system. *Top row* Interaction

energies over simulation time between all OP215 peptides and all SC lipids (OP215-SC). *Bottom row* Interaction energies between each of the OP215 peptides and all SC lipids (OP215_A-SC and OP215_B-SC). “Coul”: coulombic interaction between charged atoms. “LJ”: van der Waals between all atoms. “Total”: sum of Coul and LJ energies. (**c**) OP215 with CH-9 system. *Top row* Interaction energies over simulation time between all OP215 peptides and all SC lipids (OP215-SC), between all CH-9 peptides and all SC lipids (CH-9-SC), and between all OP215 and all CH-9 (OP215-CH9). *Bottom row* Interaction energies between each of the OP215 peptides and all SC lipids (OP215_A-SC and OP215_B-SC), and between selected CH-9 (copy 1 and 7) and all SC lipids (CH-9_1-SC and CH-9_7-SC).

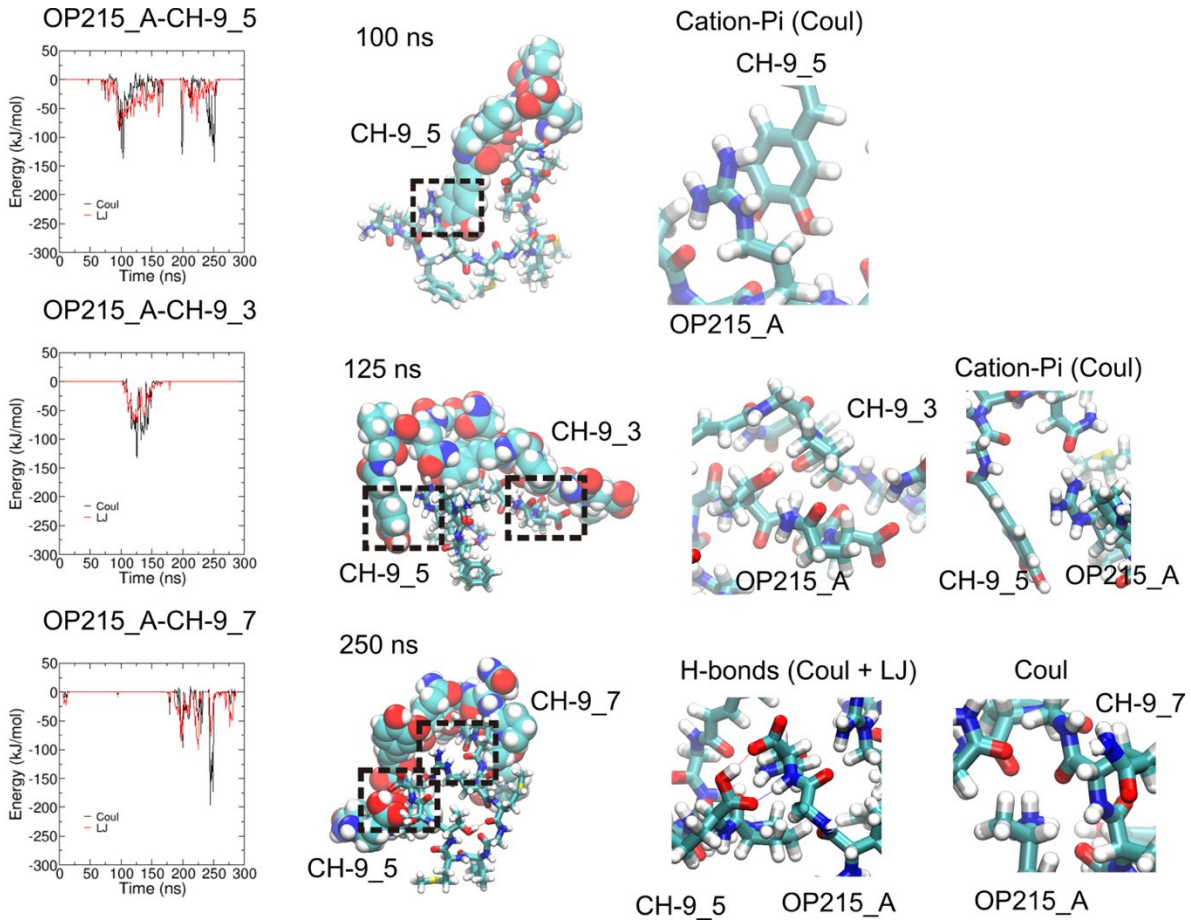


Figure S2. OP215 and CH-9 interaction energies and co-cluster snapshots for the first copy of OP215. *Left* Interaction energies over simulation time between OP215 peptide copy A and CH-9 peptides that showed strong interaction. *Right* Simulation snapshots over simulation time (OP215 in sticks and CH-9 in vdW spheres) showing inter-peptide interactions (zoomed-in views from regions marked by dashed boxes) that might have given rise to the strong interaction "windows" shown on the left. Coulombic and vdW interactions contribute similarly to the inter-peptide interactions. Cation-Pi interaction (positively charged Arg side-chain and negatively charged caffeoyl-ring) and hydrogen-bonding are observed.

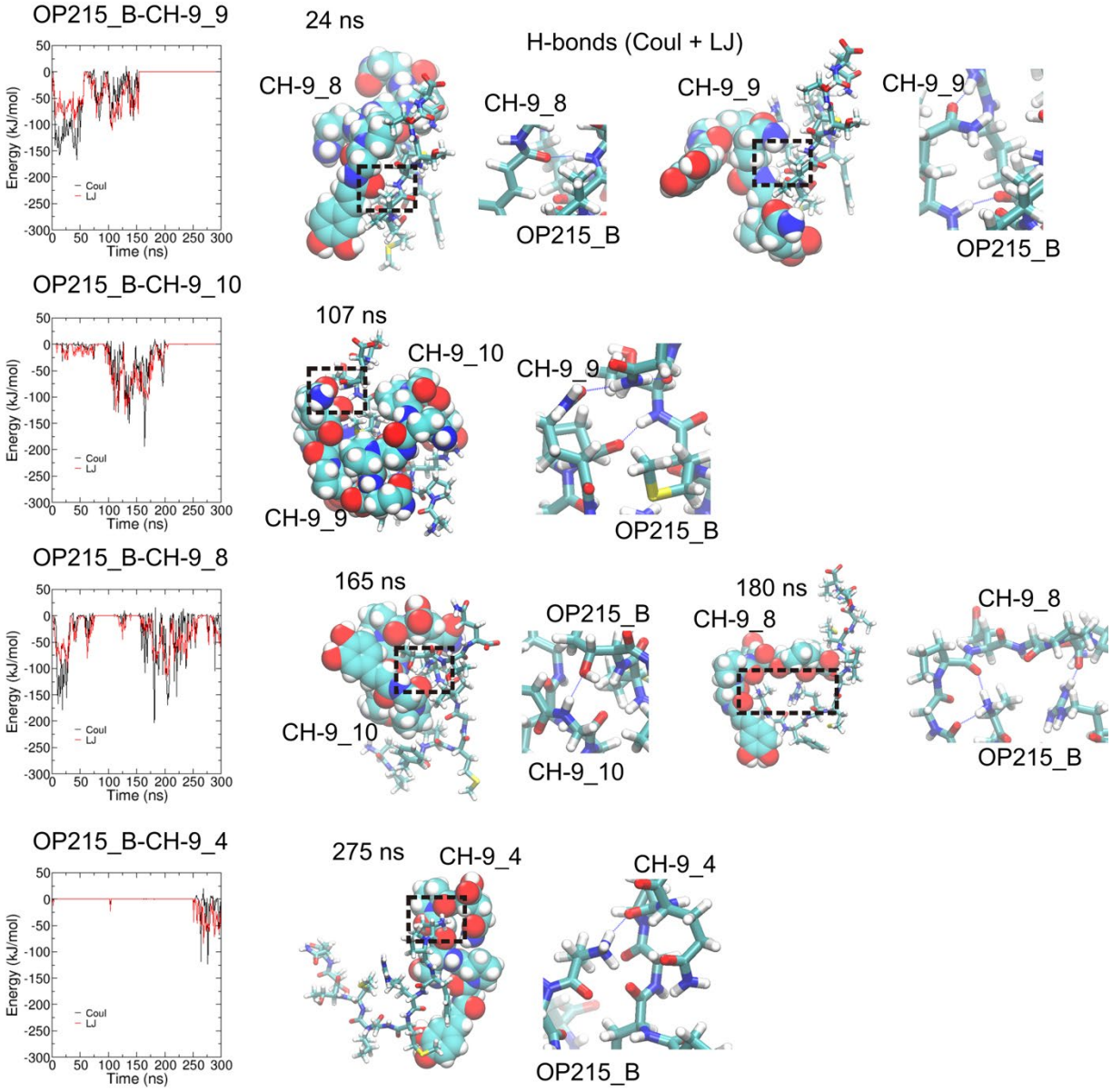


Figure S3. OP215 and CH-9 interaction energies and co-cluster snapshots for the second copy of OP215. *Left* Interaction energies over simulation time between OP215 peptide copy B and CH-9 peptides that showed strong interaction. *Right* Simulation snapshots over simulation time (OP215 in sticks and CH-9 in vdW spheres) showing inter-peptide interactions (zoomed-in views from regions marked by dashed boxes) that might have given rise to the strong interaction "windows" shown on the left.

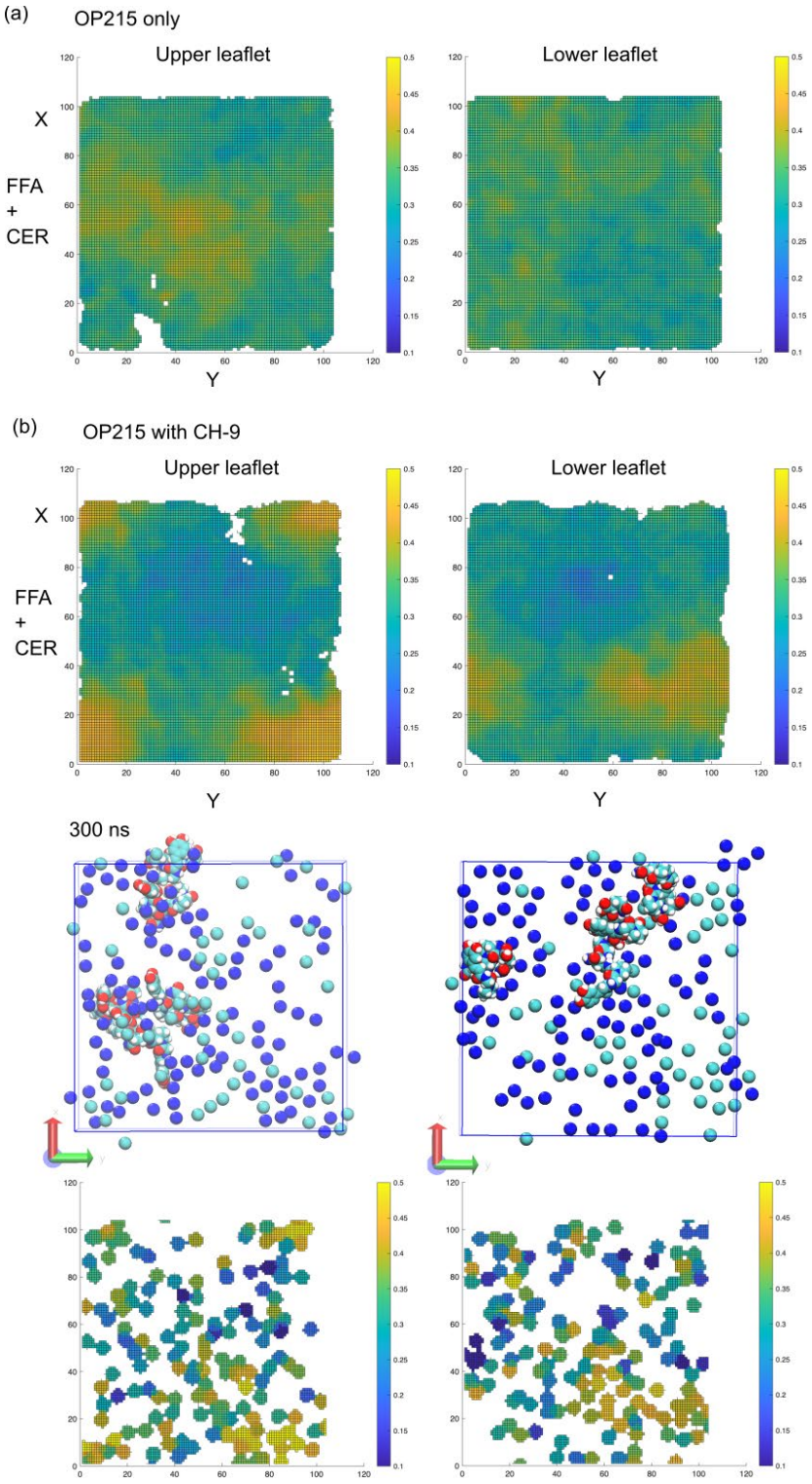


Figure S4. Spatial (2D) lipid order parameter maps using 200-300 ns of simulation data for (a) OP215-only and (b) OP215 with CH-9 systems using MOSAICS software. FFA and ceramides are used for the lipid order calculations. Simulation snapshots from 300 ns are shown for OP215 with CH-9 systems to indicate location of CH-9 on the SC

bilayer surfaces and correlate (broadly) with lower lipid order on the 2D maps at 300 ns (below simulation snapshots). In the simulation snapshot, cyan spheres are the head-group carbon atom of each FFA and blue spheres are the two head-group carbon atoms of each ceramide (two chains each) in each leaflet.

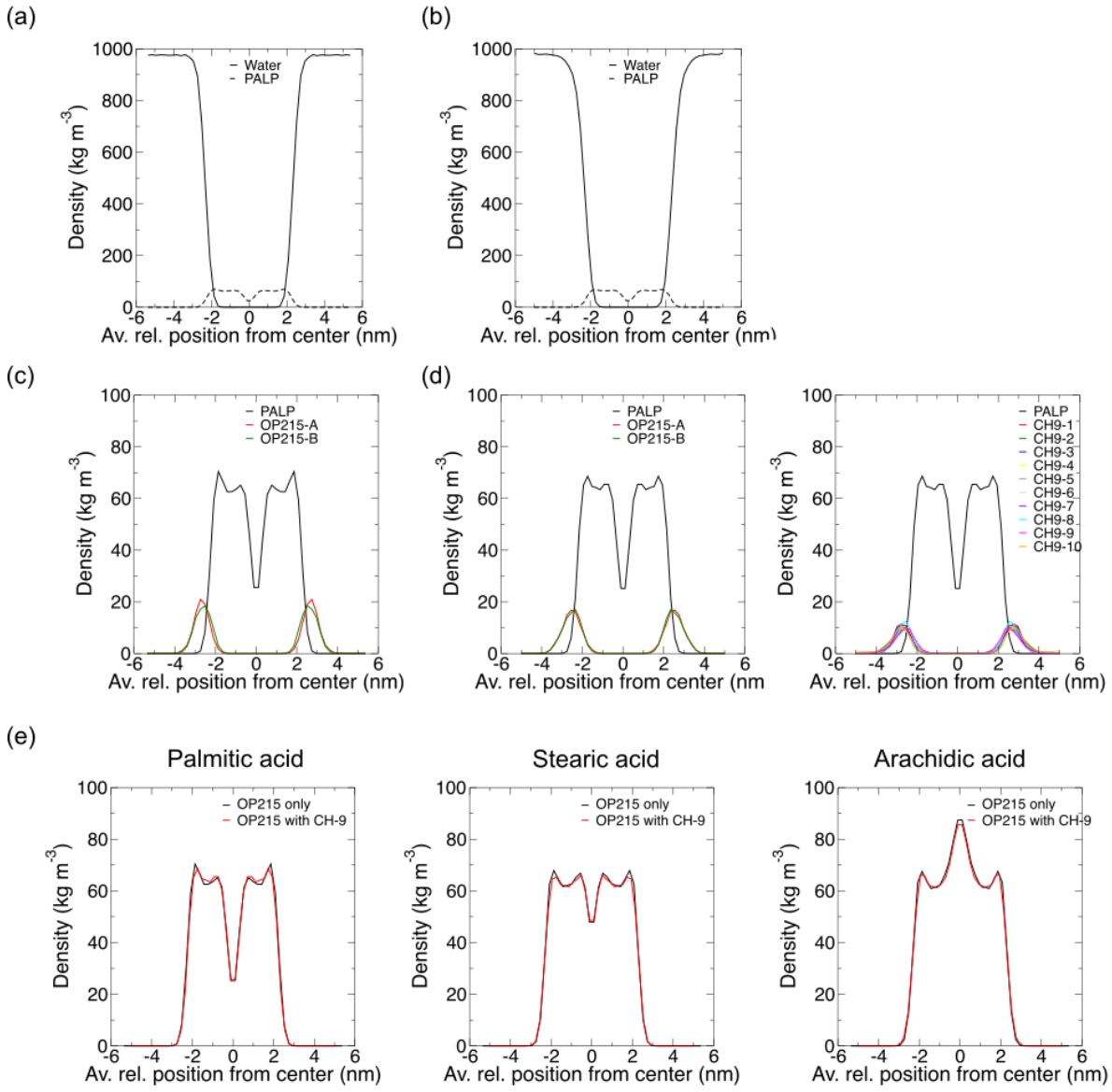


Figure S5. Mass density profiles. (a, b) Water density for (a) OP215 only and (b) OP215 with CH-9 systems over 200-300 ns. Dashed lines are density profiles for palmitic acid (PALP) to indicate density of the SC lipid bilayer. (c, d) Peptide densities together with palmitic acid to indicate the bilayer location. (e) Comparing FFA densities for OP215 only and OP215 with CH-9 systems over 200-300 ns.

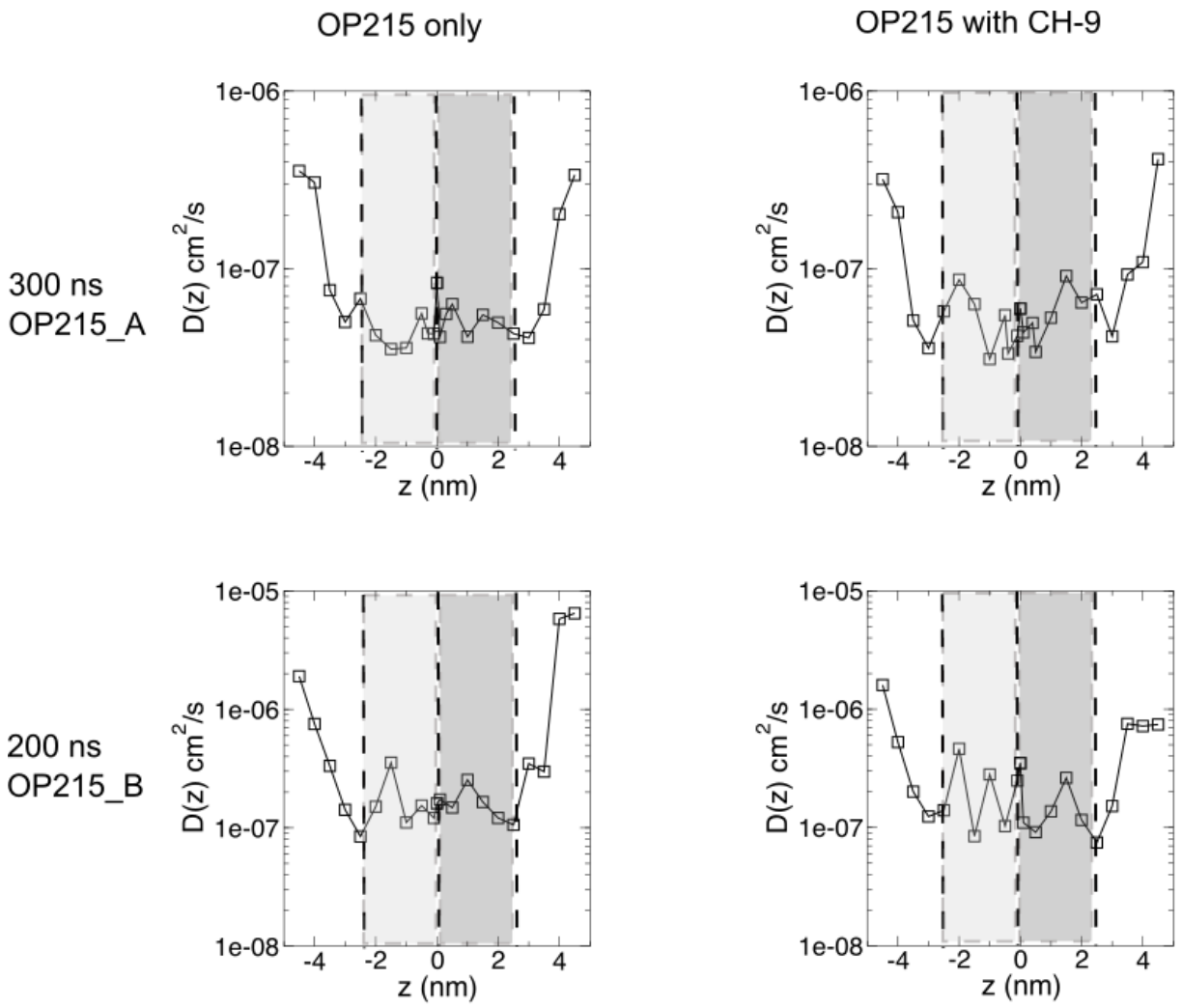


Figure S6. Comparison of the diffusivity profiles across the SC lipid bilayer for OP215 peptides in the absence (Left) and presence of CH-9 peptides (Right) using the 300 ns and 200 ns configurations from the respective simulations. The distance to the peptide center-of-mass from the center of the lipid bilayer is denoted by z. OP215_A and OP215_B denote the two copies of OP215 in each system. Dashed lines mark the location of z = –2.5 nm, 0 nm and 2.5 nm, where the areas under the profile from –2.5 nm to 0 nm (light gray) and from 0 nm to 2.5 nm (dark gray) are used to obtain the effective diffusivities.